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0424

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## RAW SEQUENCE LISTING

DATE: 04/26/2002

PATENT APPLICATION: US/10/067,457

TIME: 14:27:58

Input Set : N:\Crif3\RULE60\10067457.raw

Output Set: N:\CRF3\04262002\J067457.raw

1 <110> APPLICANT: Aventis Pharma Deutschland GmbH  
2 <120> TITLE OF INVENTION: Process for identifying substances which modulate the  
3 activity of hyperpolarization-activated cation channels  
4 <130> FILE REFERENCE: AVE D-2000/A006  
5 <140> CURRENT APPLICATION NUMBER: 10/067,457  
6 <141> CURRENT FILING DATE: 2002-04-09  
8 <150> PRIOR APPLICATION NUMBER: US/09/779,587  
9 <151> PRIOR FILING DATE: 2001-02-09  
13 <160> NUMBER OF SEQ ID NOS: 10  
14 <170> SOFTWARE: PatentIn Ver. 2.1  
16 <210> SEQ ID NO: 1  
17 <211> LENGTH: 889  
18 <212> TYPE: PRT  
19 <213> ORGANISM: Homo sapiens  
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22 1 5 10 15  
23 Ser Pro Thr Thr Gly Pro Pro Pro Pro Pro Pro Pro Arg Pro Pro Lys  
24 20 25 30  
25 Gln Gln Pro Pro Pro Pro Pro Pro Ala Pro Pro Pro Gly Pro Gly  
26 35 40 45  
27 Pro Ala Pro Pro Gln His Pro Pro Arg Ala Glu Ala Leu Pro Pro Glu  
28 50 55 60  
29 Ala Ala Asp Glu Gly Gly Pro Arg Gly Arg Leu Arg Ser Arg Asp Ser  
30 65 70 75 80  
31 Ser Cys Gly Arg Pro Gly Thr Pro Gly Ala Ala Ser Thr Ala Lys Gly  
32 85 90 95  
33 Ser Pro Asn Gly Glu Cys Gly Arg Gly Glu Pro Gln Cys Ser Pro Ala  
34 100 105 110  
35 Gly Pro Glu Gly Pro Ala Arg Gly Pro Lys Val Ser Phe Ser Cys Arg  
36 115 120 125  
37 Gly Ala Ala Ser Gly Pro Ala Pro Gly Pro Gly Pro Ala Glu Glu Ala  
38 130 135 140  
39 Gly Ser Glu Glu Ala Gly Pro Ala Gly Glu Pro Arg Gly Ser Gln Ala  
40 145 150 155 160  
41 Ser Phe Met Gln Arg Gln Phe Gly Ala Leu Leu Gln Pro Gly Val Asn  
42 165 170 175  
43 Lys Phe Ser Leu Arg Met Phe Gly Ser Gln Lys Ala Val Glu Arg Glu  
44 180 185 190  
45 Gln Glu Arg Val Lys Ser Ala Gly Ala Trp Ile Ile His Pro Tyr Ser  
46 195 200 205  
47 Asp Phe Arg Phe Tyr Trp Asp Phe Thr Met Leu Leu Phe Met Val Gly  
48 210 215 220

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49  Asn Leu Ile Ile Ile Pro Val Gly Ile Thr Phe Phe Lys Asp Glu Thr
50  225                230                235                240
51  Thr Ala Pro Trp Ile Val Phe Asn Val Val Ser Asp Thr Phe Phe Leu
52                245                250                255
53  Met Asp Leu Val Leu Asn Phe Arg Thr Gly Ile Val Ile Glu Asp Asn
54                260                265                270
55  Thr Glu Ile Ile Leu Asp Pro Glu Lys Ile Lys Lys Lys Tyr Leu Arg
56                275                280                285
57  Thr Trp Phe Val Val Asp Phe Val Ser Ser Ile Pro Val Asp Tyr Ile
58                290                295                300
59  Phe Leu Ile Val Glu Lys Gly Ile Asp Ser Glu Val Tyr Lys Thr Ala
60  305                310                315                320
61  Arg Ala Leu Arg Ile Val Arg Phe Thr Lys Ile Leu Ser Leu Leu Arg
62                325                330                335
63  Leu Leu Arg Leu Ser Arg Leu Ile Arg Tyr Ile His Gln Trp Glu Glu
64                340                345                350
65  Ile Phe His Met Thr Tyr Asp Leu Ala Ser Ala Val Met Arg Ile Cys
66                355                360                365
67  Asn Leu Ile Ser Met Met Leu Leu Leu Cys His Trp Asp Gly Cys Leu
68                370                375                380
69  Gln Phe Leu Val Pro Met Leu Gln Asp Phe Pro Arg Asn Cys Trp Val
70  385                390                395                400
71  Ser Ile Asn Gly Met Val Asn His Ser Trp Ser Glu Leu Tyr Ser Phe
72                405                410                415
73  Ala Leu Phe Lys Ala Met Ser His Met Leu Cys Ile Gly Tyr Gly Arg
74                420                425                430
75  Gln Ala Pro Glu Ser Met Thr Asp Ile Trp Leu Thr Met Leu Ser Met
76                435                440                445
77  Ile Val Gly Ala Thr Cys Tyr Ala Met Phe Ile Gly His Ala Thr Ala
78                450                455                460
79  Leu Ile Gln Ser Leu Asp Ser Ser Arg Arg Gln Tyr Gln Glu Lys Tyr
80  465                470                475                480
81  Lys Gln Val Glu Gln Tyr Met Ser Phe His Lys Leu Pro Ala Asp Phe
82                485                490                495
83  Arg Gln Lys Ile His Asp Tyr Tyr Glu His Arg Tyr Gln Gly Lys Met
84                500                505                510
85  Phe Asp Glu Asp Ser Ile Leu Gly Glu Leu Asn Gly Pro Leu Arg Glu
86                515                520                525
87  Glu Ile Val Asn Phe Asn Cys Arg Lys Leu Val Ala Ser Met Pro Leu
88                530                535                540
89  Phe Ala Asn Ala Asp Pro Asn Phe Val Thr Ala Met Leu Thr Lys Leu
90  545                550                555                560
91  Lys Phe Glu Val Phe Gln Pro Gly Asp Tyr Ile Ile Arg Glu Gly Thr
92                565                570                575
93  Ile Gly Lys Lys Met Tyr Phe Ile Gln His Gly Val Val Ser Val Leu
94                580                585                590
95  Thr Lys Gly Asn Lys Glu Met Lys Leu Ser Asp Gly Ser Tyr Phe Gly
96                595                600                605
97  Glu Ile Cys Leu Leu Thr Arg Gly Arg Arg Thr Ala Ser Val Arg Ala

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98          610          615          620
99  Asp Thr Tyr Cys Arg Leu Tyr Ser Leu Ser Val Asp Asn Phe Asn Glu
100      625          630          635          640
101  Val Leu Glu Glu Tyr Pro Met Met Arg Arg Ala Phe Glu Thr Val Ala
102          645          650          655
103  Ile Asp Arg Leu Asp Arg Ile Gly Lys Lys Asn Ser Ile Leu Leu His
104          660          665          670
105  Lys Val Gln His Asp Leu Asn Ser Gly Val Phe Asn Asn Gln Glu Asn
106          675          680          685
107  Ala Ile Ile Gln Glu Ile Val Lys Tyr Asp Arg Glu Met Val Gln Gln
108      690          695          700
109  Ala Glu Leu Gly Gln Arg Val Gly Leu Phe Pro Pro Pro Pro Pro
110      705          710          715          720
111  Pro Gln Val Thr Ser Ala Ile Ala Thr Leu Gln Gln Ala Ala Ala Met
112          725          730          735
113  Ser Phe Cys Pro Gln Val Ala Arg Pro Leu Val Gly Pro Leu Ala Leu
114          740          745          750
115  Gly Ser Pro Arg Leu Val Arg Arg Pro Pro Pro Gly Pro Ala Pro Ala
116          755          760          765
117  Ala Ala Ser Pro Gly Pro Pro Pro Pro Ala Ser Pro Pro Gly Ala Pro
118          770          775          780
119  Ala Ser Pro Arg Ala Pro Arg Thr Ser Pro Tyr Gly Gly Leu Pro Ala
120      785          790          795          800
121  Ala Pro Leu Ala Gly Pro Ala Leu Pro Ala Arg Arg Leu Ser Arg Ala
122          805          810          815
123  Ser Arg Pro Leu Ser Ala Ser Gln Pro Ser Leu Pro His Gly Ala Pro
124          820          825          830
125  Gly Pro Ala Ala Ser Thr Arg Pro Ala Ser Ser Ser Thr Pro Arg Leu
126          835          840          845
127  Gly Pro Thr Pro Ala Ala Arg Ala Ala Ala Pro Ser Pro Asp Arg Arg
128          850          855          860
129  Asp Ser Ala Ser Pro Gly Ala Ala Gly Gly Leu Asp Pro Gln Asp Ser
130      865          870          875          880
131  Ala Arg Ser Arg Leu Ser Ser Asn Leu
132          885

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134 &lt;210&gt; SEQ ID NO: 2

135 &lt;211&gt; LENGTH: 3372

136 &lt;212&gt; TYPE: DNA

137 &lt;213&gt; ORGANISM: Homo sapiens

138 &lt;400&gt; SEQUENCE: 2

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139  cggctccgct ccgcactgcc cggcgccgcc tcgccatgga cgcgcgcggg ggcggcgggc 60
140  ggcccgggga gagcccgggc gcgagcccca cgaccgggac gccgcgcgcg ccgcccccg 120
141  gcccccccaa acagcagccg ccgcgcgcgc cgccgcccgc gcccccccg ggcggcgggc 180
142  ccgcgcccc ccagcaccgc ccccgggccg aggcgttgcc ccgagggcg gcgatgagg 240
143  gcggcccgcg gggccggctc cgcagccgcg acagctcgtg cggccgcccc ggcaccccg 300
144  gcgcggcgag cacggccaag ggcagccga acggcgagt gcggcgcggc gagccgcagt 360
145  gcagccccgc ggggcccgcg gggcgccgc gggggcccaa ggtgtcgttc tcgtgccgcg 420
146  gggcgccctc ggggcccgcg ccggggccgc ggcggcgga ggagggggc agcaggagg 480
147  cgggcccggc gggggagccg cgcggcagcc aggcagctt catgcagcgc cagttcggcg 540

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148   cgctcctgca gccggggcgtc aacaagttct cgctgcggat gttcggcagc cagaaggccg 600
149   tggagcgcgga gcaggagcgc gtcaagtcgg cgggggcctg gatcatccac ccgtacagcg 660
150   acttcagggtt ctactgggac ttcacatgc tgcgtttcat ggtgggaaac ctcacatca 720
151   tcccagtggt catcaccttc ttcaaggatg agaccactgc cccgtggatc gtgttcaacg 780
152   tgggtctcgga caccttcttc ctcatggacc tgggtgttgaa cttccgcacc ggcattgtga 840
153   tcgaggacaa cacggagatc atcctggacc ccgagaagat caagaagaag tatctgcgca 900
154   cgtggttcgt ggtggacttc gtgtcctcca tccccgtgga ctacatcttc cttatcgtgg 960
155   agaagggcat tgactccgag gtctacaaga cggcacgcgc cctgcgcacg gtgcgcttca 1020
156   ccaagatcct cagcctcctg cggctgctgc gcctctcacg cctgatccgc tacatccatc 1080
157   agtgggagga gatcttccac atgacctatg acctggccag cgcggtgatg aggatctgca 1140
158   atctcatcag catgatgctg ctgctctgcc actgggacgg ctgcctgcag ttctcgtgct 1200
159   ctatgctgca ggacttcccg cgcaactgct ggggtgtccat caatggcatg gtgaaccact 1260
160   cgtggagtga actgtactcc ttgcactct tcaaggccat gagccacatg ctgtgcacog 1320
161   ggtacggcgg gcaggcgccc gagagcatga cggacatctg gctgaccatg ctcagcatga 1380
162   ttgtgggtgc cacctgctac gccatgttca tcggccacgc cactgccctc atccagtcgc 1440
163   tggactcttc gcggcgccag taccaggaga agtacaagca ggtggagcag tacatgtcct 1500
164   tccacaagct gccagctgac ttccgccaga agatccacga ctactatgag caccgttacc 1560
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167   accccaactt cgtcacggcc atgctgacca agctcaagtt cgaggtcttc cagcggggtg 1740
168   actacatcat ccgcaaggcc accatcgga agaagatgta cttcatccag caccgctggg 1800
169   tcagcgtgct cactaaggcc aacaaggaga tgaagctgtc cgatggctcc tacttcgggg 1860
170   agatctgctt gctcaccgcg gcccgccgca cggcgagcgt gcgggctgac acctactgcc 1920
171   gcctctatct gctgagcgtg gacaacttca acgaggtgct ggaggagtac cccatgatgc 1980
172   ggcgcgccct cgagacggtg gccatcgacc gcctggaccg catcggaag aagaattcca 2040
173   tcctcctgca caagtgagc catgacctca actcgggcgt attcaacaac caggagaacg 2100
174   ccatcatcca ggagatcgtc aagtacgacc gcgagatggt gcagcaggcc gagctgggtc 2160
175   agcgcgtggg cctcttcccg ccgcccgcgc cgcgcgcgca ggtcacctcg gccatcgcca 2220
176   cgctgcagca ggcggcgccc atgagcttct gcccgaggt ggcgcggccg ctcggtgggg 2280
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179   caccgcggac ctgcacctac ggcggcctgc ccgcgcgcc ccttgcctgg ccgcacctgc 2460
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181   acggcgcccc cggccccgcg gcccccacac gcccgccag cagctccaca ccgcgcttgg 2580
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183   ccggcgccgc cggcggcctg gacccccagg actccgcgc ctgcgcctc tcgtccaa 2700
184   tgtgaccttc gccgaccgcc ccgcgggccc aggcgggccc ggggcggggc cgtcatccag 2760
185   accaaagcca tgccattgcg ctgccccggc cgccagtcgg ccagaagcc atagacgaga 2820
186   cgtaggtagc cgtagttgga cggacgggca gggcgggcgg ggcagcccc tcgcgcccc 2880
187   cggccgtccc cctcatcgcc ccgcgcgcca ccccatcgcc cctgcccccc ggcggcgccc 2940
188   tcgctgagca gggggtctcc ttcaactcgg tgctcagtt ccccgagctg taagacagg 3000
189   acggggcggc ccagtggctg agaggagccg gctgtggagc ccgcgccgc cccaccctc 3060
190   taggtggccc ccgtccgagg aggatcgttt tctaagtga atacttgcc cgcggcttc 3120
191   ccgtgcccc catcgcgctc acgcaataac cggccccg ccgcgtccgc cgcgtcccc 3180
192   ggtgacctcg gggagcagca cccgcctcc ctccagcact ggcaccgaga ggcaggcctg 3240
193   gctgcgcagg gcgcgggggg gaggtgggg tccgcgcgc gtgatgaatg tactgacgag 3300
194   ccgaggcagc agtgccccca ccgtggcccc ccacgcccc ttaaccccc cacccccatt 3360
195   ccgcgcaata aa 3372
197 <210> SEQ ID NO: 3

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Input Set : N:\Crf3\RULE60\10067457.raw

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198 <211> LENGTH: 1203
199 <212> TYPE: PRT
200 <213> ORGANISM: Homo sapiens
201 <400> SEQUENCE: 3
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204 Gln Gln Val Gly Ala Lys Ala Trp Ile Met Asp Glu Glu Glu Asp Ala
205 20 25 30
206 Glu Glu Glu Gly Ala Gly Gly Arg Gln Asp Pro Ser Arg Arg Ser Ile
207 35 40 45
208 Arg Leu Arg Pro Leu Pro Ser Pro Ser Pro Ser Ala Ala Ala Gly Gly
209 50 55 60
210 Thr Glu Ser Arg Ser Ser Ala Leu Gly Ala Ala Asp Ser Glu Gly Pro
211 65 70 75 80
212 Ala Arg Gly Ala Gly Lys Ser Ser Thr Asn Gly Asp Cys Arg Arg Phe
213 85 90 95
214 Arg Gly Ser Leu Ala Ser Leu Gly Ser Arg Gly Gly Gly Ser Gly Gly
215 100 105 110
216 Thr Gly Ser Gly Ser Ser His Gly His Leu His Asp Ser Ala Glu Glu
217 115 120 125
218 Arg Arg Leu Ile Ala Glu Gly Asp Ala Ser Pro Gly Glu Asp Arg Thr
219 130 135 140
220 Pro Pro Gly Leu Ala Ala Glu Pro Glu Arg Pro Gly Ala Ser Ala Gln
221 145 150 155 160
222 Pro Ala Ala Ser Pro Pro Pro Pro Gln Gln Pro Pro Gln Pro Ala Ser
223 165 170 175
224 Ala Ser Cys Glu Gln Pro Ser Val Asp Thr Ala Ile Lys Val Glu Gly
225 180 185 190
226 Gly Ala Ala Ala Gly Asp Gln Ile Leu Pro Glu Ala Glu Val Arg Leu
227 195 200 205
228 Gly Gln Ala Gly Phe Met Gln Arg Gln Phe Gly Ala Met Leu Gln Pro
229 210 215 220
230 Gly Val Asn Lys Phe Ser Leu Arg Met Phe Gly Ser Gln Lys Ala Val
231 225 230 235 240
232 Glu Arg Glu Gln Glu Arg Val Lys Ser Ala Gly Phe Trp Ile Ile His
233 245 250 255
234 Pro Tyr Ser Asp Phe Arg Phe Tyr Trp Asp Leu Thr Met Leu Leu Leu
235 260 265 270
236 Met Val Gly Asn Leu Ile Ile Ile Pro Val Gly Ile Thr Phe Phe Lys
237 275 280 285
238 Asp Glu Asn Thr Thr Pro Trp Ile Val Phe Asn Val Val Ser Asp Thr
239 290 295 300
240 Phe Phe Leu Ile Asp Leu Val Leu Asn Phe Arg Thr Gly Ile Val Val
241 305 310 315 320
242 Glu Asp Asn Thr Glu Ile Ile Leu Asp Pro Gln Arg Ile Lys Met Lys
243 325 330 335
244 Tyr Leu Lys Ser Trp Phe Met Val Asp Phe Ile Ser Ser Ile Pro Val
245 340 345 350
246 Asp Tyr Ile Phe Leu Ile Val Glu Thr Arg Ile Asp Ser Glu Val Tyr

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/067,457

DATE: 04/26/2002

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